IN THE CLAIMS

Please amend claims 15, 28, 51 – 54, and 57-60. Please cancel claims 1-4, 16-20, 22-27, 31 – 50, 55, and 56.

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. – 14. (Canceled)

15. (Currently amended) A method of binding [[a]] an isolated or recombinant DmGPCR with a DmGPCR binding partner comprising the steps of: contacting a composition comprising a DmGPCR with a DmGPCR binding partner; and allowing said DmGPCR binding partner to bind said DmGPCR wherein said DmGPCR is an amino cid sequence encoded by DmGPCR7 (SEQ ID NO: 17) and wherein said DmGPCR binding partner is a leucokinin (LK).

16. – 20. (Canceled)

21. (Previously presented) The method according to claim 20, wherein said leucokinin has a sequence with at least 80% sequence identity to a sequence selected from the group consisting of LK-I (SEQ ID NO: 175), LK-V (SEQ ID NO: 176), LK-VI (SEQ ID NO: 177), and LK-VIII (SEQ ID NO: 178), Culekinin (SEQ ID NO: 179), LY7MMaca lymnolçinin (SEQ ID NO: 180), DLK-1 (SEQ ID NO : 181), DLK-2 (SEQ ID NO: 182), and DLK-2a (SEQ ID NO: 183).

22. – 27. (Canceled)

28. (Currently amended) A method for identifying a modulator of binding and/or function between a DmGPCR and a DmGPCR binding partner, comprising the steps of :

contacting a DmGPCR binding partner and a composition comprising a DmGPCR in the presence or in the absence of a putative modulator compound; detecting binding between the DmGPCR binding partner and the DmGPCR ; and determining whether binding in the presence of said putative modulator compound is increased or decreased compared to binding in the absence of said putative modulator compound, determining whether function in the presence of said putative modulator compound is increased or decreased compared to function in the absence of said putative modulator compound, wherein said DmGPCR is an amino acid sequence encoded by DmGPCR7 (SEQ ID NO: 17).

29. (Original) The method according to claim 28, wherein said DmGPCR binding partner is a leucokinin.

30. (Original) The method according to claim 29, wherein said leucokinin has a sequence with at least 80% sequence identity to a sequence selected from the group consisting of LK-I (SEQ ID NO: 175), LK-V (SEQ ID NO: 176), LK-VI (SEQ ID NO: 177), LK-VIII (SEQ ID NO: 178), Culekinin (SEQ ID NO: 179), Ly7linaea lynmokinin (SEQ ID NO: 180), DLK-1 (SEQ ID NO: 181), DLK-2 (SEQ ID NO: 182), and DLK-2a (SEQ ID NO: 183).

31. – 50. (Canceled)

51. (Currently amended) The method of claim [[49]] 28 wherein said DmGPCR and said DmGPCR binding partner are selected from the group consisting of:

~~DmGPCR1 and a DmGPCR1 binding partner has a sequence with at least 90% sequence identity to a sequence selected from the group consisting of SEQ ID NO:186 and SEQ ID NO:187;~~

~~DmGPCR5 and a drotachykinin that has a sequence with at least 90% sequence identity to a sequence selected from the group consisting of DTK-1 (SEQ ID~~

~~NO:169), Met8-DTK-2 (SEQ ID NO:170), DTK-2 (SEQ ID NO:171), DTK-3 (SEQ ID NO:172), DTK-4 (SEQ ID NO:173), and DTK-5 (SEQ ID NO:174);~~

DmGPCR7 and a leucokinin that has a sequence with at least 90% sequence identity to a sequence selected from the group consisting of LK-I (SEQ ID NO:175), LK-V (SEQ ID NO:176), LK-VI (SEQ ID NO:177), LK-VIII (SEQ ID NO:178), Culekinin (SEQ ID NO:179), Ly7linaca lynmokinin (SEQ ID NO:180), DLK-1 (SEQ ID NO:181), DLK-2 (SEQ ID NO:182), and DLK-2a (SEQ ID NO:183)~~; and~~

~~DmGPCR8 and an allatostatin that has a sequence with at least 90% sequence identity to a sequence selected from the group consisting of AST-C (SEQ ID NO: 184) and DST-C (SEQ ID NO:185).~~

52. (Currently amended) The method of claim [[49]] 28 wherein said DmGPCR and said DmGPCR binding partner are selected from the group consisting of:

~~DmGPCR1 and a DmGPCR1 binding partner has a sequence with at least 95% sequence identity to a sequence selected from the group consisting of SEQ ID NO: 186 and SEQ ID NO : 187;~~

~~DmGPCR5 and a drotachykinin that has a sequence with at least 95% sequence identity to a sequence selected from the group consisting of DTK-1 (SEQ ID NO:169), Met8-DTK-2 (SEQ ID NO:170), DTK-2 (SEQ ID NO:171), DTK-3 (SEQ ID NO:172), DTK-4 (SEQ ID NO:173), and DTK-5 (SEQ ID NO:174);~~

DmGPCR7 and a leucokinin that has a sequence with at least 95% sequence identity to a sequence selected from the group consisting of LK-I (SEQ ID NO:175), LK-V (SEQ ID NO:176), LK-VI (SEQ ID NO:177), LK-VIII (SEQ ID NO:178), Culekinin (SEQ ID NO:179), Ly7linaca lynmokinin (SEQ ID NO:180), DLK-1 (SEQ ID NO:181), DLK-2 (SEQ ID NO:182), and DLK-2a (SEQ ID NO:183)~~; and~~

~~DmGPCR8 and an allatostatin that has a sequence with at least 95% sequence identity to a sequence selected from the group consisting of AST-C (SEQ ID NO:184) and DST-C (SEQ ID NO:185).~~

53. (Currently amended) The method of claim [[49]] 28 wherein said DmGPCR and said DmGPCR binding partner are selected from the group consisting of:

~~DmGPCR1 and a DmGPCR1 binding partner has a sequence with at least 99% sequence identity to a sequence selected from the group consisting of SEQ ID NO: 186 and SEQ ID NO:187;~~

~~DmGPCR5 and a drotachykinin that has a sequence with at least 99% sequence identity to a sequence selected from the group consisting of DTK-1 (SEQ ID NO:169), Met8-DTK-2 (SEQ ID NO:170), DTK-2 (SEQ ID NO:171), DTK-3 (SEQ ID NO:172), DTK-4 (SEQ ID NO:173), and DTK-5 (SEQ ID NO:174);~~

DmGPCR7 and a leucokinin that has a sequence with at least 99% sequence identity to a sequence selected from the group consisting of LK-I (SEQ ID NO:175), LK-V (SEQ ID NO:176), LK-VI (SEQ ID NO:177), LK-VIII (SEQ ID NO: 178), Culekinin (SEQ ID NO:179), Ly7linaca lynmokinin (SEQ ID NO:180), DLK-1 (SEQ ID NO:181), DLK-2 (SEQ ID NO:182), and DLK-2a (SEQ ID NO:183)~~; and~~

~~DmGPCR8 and an allatostatin that has a sequence with at least 99% sequence identity to a sequence selected from the group consisting of AST-C (SEQ ID NO:184) and DST-C (SEQ ID NO:185).~~

54. (Currently amended) The method of claim [[49]] 28 wherein said DmGPCR and said DmGPCR binding partner are ~~selected from the group consisting of:~~

~~DmGPCR1 and a DmGPCR1 binding partner has a sequence selected from the group consisting of SEQ ID NO:186 and SEQ ID NO:187;~~

~~DmGPCR5 and a drotachykinin that has a sequence selected from the group consisting of DTK-1 (SEQ ID NO:169), Met8-DTK-2 (SEQ ID NO:170), DTK-2 (SEQ ID NO:171), DTK-3 (SEQ ID NO:172), DTK-4 (SEQ ID NO:173), and DTK-5 (SEQ ID NO:174);~~

DmGPCR7 and a leucokinin that has a sequence selected from the group consisting of LK-I (SEQ ID NO:175), LK-V (SEQ ID NO:176), LK-VI (SEQ ID NO:177), LK-VIII (SEQ ID NO:178), Culekinin (SEQ ID NO:179), Ly7linaca lynmokinin (SEQ ID NO:180), DLK-1 (SEQ ID NO:181), DLK-2 (SEQ ID NO:182), and DLK-2a (SEQ ID NO:183)~~; and~~

~~DmGPCR8 and an allatostatin that has a sequence selected from the group consisting of AST-C (SEQ ID NO:184) and DST-C (SEQ ID NO:185).~~

55. – 56. (Canceled)

57. (Currently amended) The method according to claim 15, wherein said DmGPCR and said DmGPCR binding partner is selected from the group consisting of:

~~DmGPCR1 and a DmGPCR1 binding partner has a sequence with at least 90% sequence identity to a sequence selected from the group consisting of SEQ ID NO:186 and SEQ ID NO:187;~~

~~DmGPCR5 and a drotachykinin that has a sequence with at least 90% sequence identity to a sequence selected from the group consisting of DTK-1 (SEQ ID NO:169), Met8-DTK-2 (SEQ ID NO:170), DTK-2 (SEQ ID NO:171), DTK-3 (SEQ ID NO:172), DTK-4 (SEQ ID NO:173), and DTK-5 (SEQ ID NO:174);~~

DmGPCR7 and a leucokinin that has a sequence with at least 90% sequence identity to a sequence selected from the group consisting of LK-I (SEQ ID NO:175), LK-V (SEQ ID NO:176), LK-VI (SEQ ID NO:177), LK-VIII (SEQ ID NO:178), Culekinin (SEQ ID NO:179), Ly7linaca lynmokinin (SEQ ID NO:180), DLK-1 (SEQ ID NO:181), DLK-2 (SEQ ID NO:182), and DLK-2a (SEQ ID NO:183)~~; and~~

~~DmGPCR8 and an allatostatin that has a sequence with at least 90% sequence identity to a sequence selected from the group consisting of AST-C (SEQ ID NO:184) and DST-C (SEQ ID NO:185).~~

58. (Currently amended) The method according to claim 15, wherein said DmGPCR and said DmGPCR binding partner is selected from the group consisting of:

~~DmGPCR1 and a DmGPCR1 binding partner has a sequence with at least 95% sequence identity to a sequence selected from the group consisting of SEQ ID NO:186 and SEQ ID NO:187;~~

~~DmGPCR5 and a drotachykinin that has a sequence with at least 95% sequence identity to a sequence selected from the group consisting of DTK-1 (SEQ ID NO:169), Met8-DTK-2 (SEQ ID NO:170), DTK-2 (SEQ ID NO:171), DTK-3 (SEQ ID NO:172), DTK-4 (SEQ ID NO:173), and DTK-5 (SEQ ID NO:174);~~

DmGPCR7 and a leucokinin that has a sequence with at least 95% sequence identity to a sequence selected from the group consisting of LK-I (SEQ ID NO:175), LK-V (SEQ ID NO:176), LK-VI (SEQ ID NO:177), LK-VIII (SEQ ID NO:178), Culekinin (SEQ ID NO:179), Ly7linaca lynmokinin (SEQ ID NO:180), DLK-1 (SEQ ID NO:181), DLK-2 (SEQ ID NO:182), and DLK-2a (SEQ ID NO:183)~~; and~~

~~DmGPCR8 and an allatostatin that has a sequence with at least 95% sequence identity to a sequence selected from the group consisting of AST-C (SEQ ID NO:184) and DST-C (SEQ ID NO:185).~~

59. (Currently amended) The method according to claim 15, wherein said DmGPCR and said DmGPCR binding partner is selected from the group consisting of:

~~DmGPCR1 and a DmGPCR1 binding partner has a sequence with at least 99% sequence identity to a sequence selected from the group consisting of SEQ ID NO:186 and SEQ ID NO:187;~~

~~DmGPCR5 and a drotachykinin that has a sequence with at least 99% sequence identity to a sequence selected from the group consisting of DTK-1 (SEQ ID NO:169), Met8-DTK-2 (SEQ ID NO:170), DTK-2 (SEQ ID NO:171), DTK-3 (SEQ ID NO:172), DTK-4 (SEQ ID NO:173), and DTK-5 (SEQ ID NO:174);~~

DmGPCR7 and a leucokinin that has a sequence with at least 99% sequence identity to a sequence selected from the group consisting of LK-I (SEQ ID NO:175), LK-V (SEQ ID NO:176), LK-VI (SEQ ID NO:177), LK-VIII (SEQ ID NO:178), Culekinin (SEQ ID NO:179), Ly7linaca lynmokinin (SEQ ID NO:180), DLK-1 (SEQ ID NO:181), DLK-2 (SEQ ID NO:182), and DLK-2a (SEQ ID NO:183)~~; and~~

~~DmGPCR8 and an allatostatin that has a sequence with at least 99% sequence identity to a sequence selected from the group consisting of AST-C (SEQ ID NO:184) and DST-C (SEQ ID NO:185)~~.

60. (Currently amended) The method according to claim 15, wherein said DmGPCR and said DmGPCR binding partner is ~~selected from the group consisting of:~~

~~DmGPCR1 and a DmGPCR1 binding partner has a sequence selected from the group consisting of SEQ ID NO:186 and SEQ ID NO:187;~~

~~DmGPCR5 and a drotachykinin that has a sequence selected from the group consisting of DTK-1 (SEQ ID NO:169), Met8-DTK-2 (SEQ ID NO:170), DTK-2 (SEQ ID NO:171), DTK-3 (SEQ ID NO:172), DTK-4 (SEQ ID NO:173), and DTK-5 (SEQ ID NO:174);~~

DmGPCR7 and a leucokinin that has a sequence selected from the group consisting of LK-I (SEQ ID NO:175), LK-V (SEQ ID NO:176), LK-VI (SEQ ID NO:177), LK-VIII (SEQ ID NO:178), Culekinin (SEQ ID NO:179), Ly7linaca lynmokinin (SEQ ID NO:180), DLK-1 (SEQ ID NO:181), DLK-2 (SEQ ID NO:182), and DLK-2a (SEQ ID NO:183)~~; and~~

~~DmGPCR8 and an allatostatin that has a sequence selected from the group consisting of AST-C (SEQ ID NO:184) and DST-C (SEQ ID NO:185)~~.